

AMENDMENT TO THE SPECIFICATION

Please replace the paragraph starting on page 20, line 19, with the following amended paragraph:

When an exon has alternative splice variants, the determination of the expression of the gene containing the exon can be aided by determining some distinguishing structural characteristics (a characteristic that distinguishes a particular exon variant from other variants of the same exon), such as the length, of the expressed variant or variants of the exon. For example, a set of polynucleotide probes of successive overlapping sequences, *i.e.*, tiled sequences, across the genomic region containing the longest known or predicted variant of an exon can be used to determine the variant or variants that are expressed. The set of polynucleotide probes can comprise successive overlapping sequences at steps of a predetermined base intervals, *e.g.* at steps of 1, 5, or 10 base intervals, span, or are tiled across, the genomic region containing the longest variant. Alternatively, a set of polynucleotide probes comprising exon specific probes and variant junction probes can be used to determine the variant or variants that are expressed. In a preferred embodiment, the exon specific probes are specifically hybridizable to the common sequences in all different variants of the exon, whereas the variant junction probes are specifically hybridizable to the different splice junction sequences of the exon.